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Figure 1a

1 MALPNKFFLW FCCFAWLCEP ISLDSLPSRG EAQIVARTAL ESEAETWSLL

R87H [E1]



51 NHLGGRHRPG LLSPLLEVLY DGHGEPRLQ PDDRALRYMK RLYKAYATKE



101 GTPKSNRRHL YNTVRLFTPC AQHKQAPGDL AAGTFPSVDL LFNLDRTVV

151 EHLFKSVLLY TFNNSISFPF PVKCICNLVI KEPEFSSKTL PRAPYSFTYN

E241K [324]



201 SQFEFRKKYK WMEIDVTAPL EPLVASHKRN IHMSVNFTCA EDQLQHPSAR

251 DSLFNMTLLV APSLLLYLND TSAQAFHRWH SLHPKRKPSQ GPDQKRGLSA

(1)

V332I [597]



301 YPVGEEAAEG VRSS[REDACTED]DQ ESASSELKKP LVPASVNLSE YFKQFLFPQN

V371M [714]



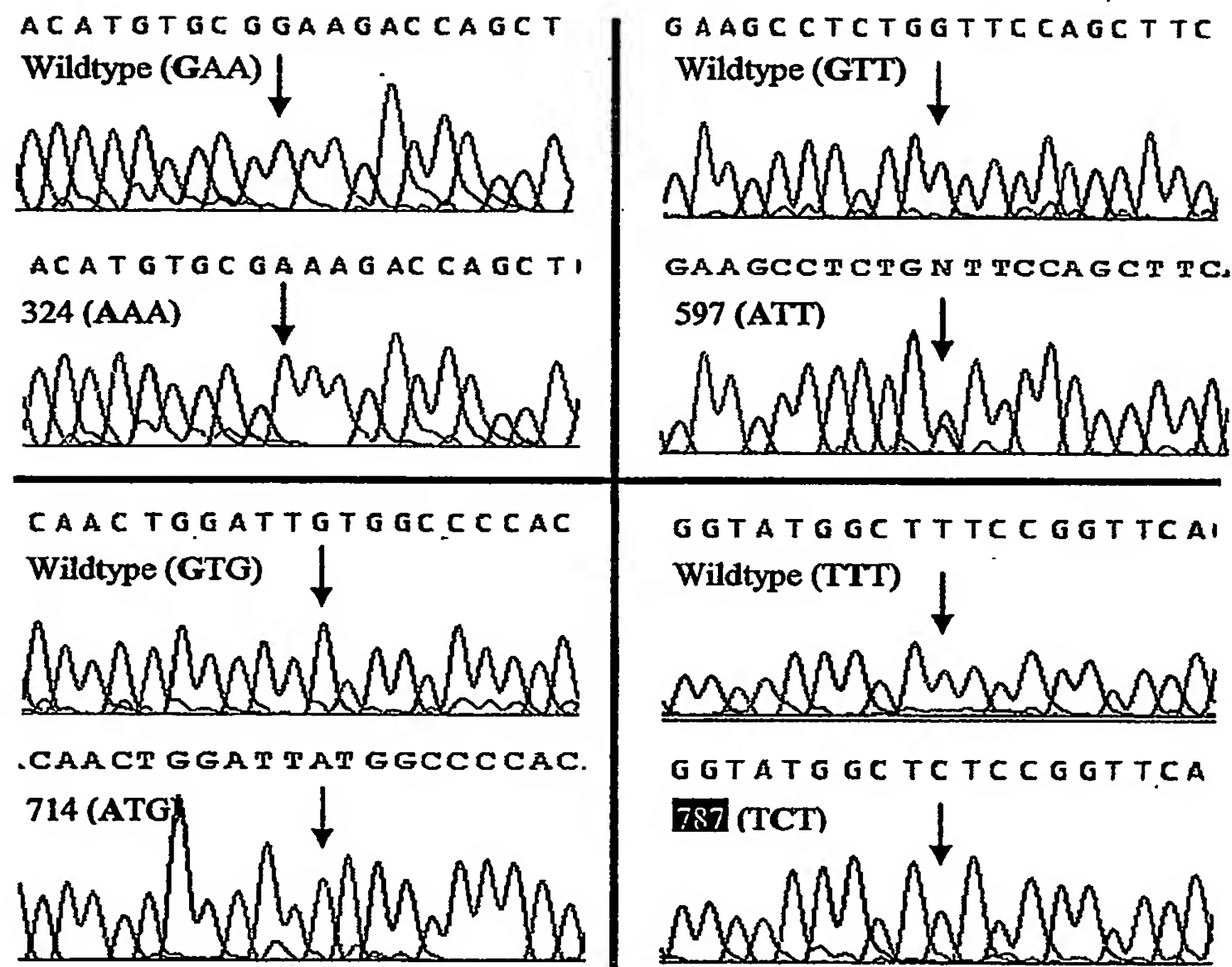
S395F [787]

351 ECELHDFRLS FSQKWDNWI VAPHKYNPRY CKGDCPRAVG HRYG[REDACTED]PVHTM

401 VQNIIEKLD SSVPRPSCVP AKYSPLSVLA IEPDGSIAYK EYEDMIATKC

(135)

Figure 1b



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Figure 2a

1 MVLLSILRIL LWGLVLFMEH RVQMTQVGQP SIAHLPEAPT LPLIQELLE
51 APGKQQRKPR VLGHPRLRYML ELYQRSADAS GHPRENRTIG ATMVRLVRPL
101 ASVARPLRGS WHIQTLDFPL RPNRVAYQLV RATVVYRHQL HLTHSHLSCH
151 VEPWVQKSPT NHFPSSGRGS SKPSLLPKTW TEMDIMEHVG QKLWNHKGRR

Q239Ter [S1]

201 VLRLRFVCQQ PRGSEVLEFW WHGTSSLDTV FLLLYFNDTQ SVQTKPLPK
(1)
251 GLKEFTEKDP SLLLEPQA GSIASEVPGP SREHDGPESN QCSLHPFQVS
301 FQQLGWDHWI IAPHLYTPNY CKGVCPRVLH YGLNSPNHAI IQNLVSELVD

S367I [S2]

(125)
351 QNVPQPSCVP YKYVPI SILL IEANGSILYK EYEGMIAQSC TCR

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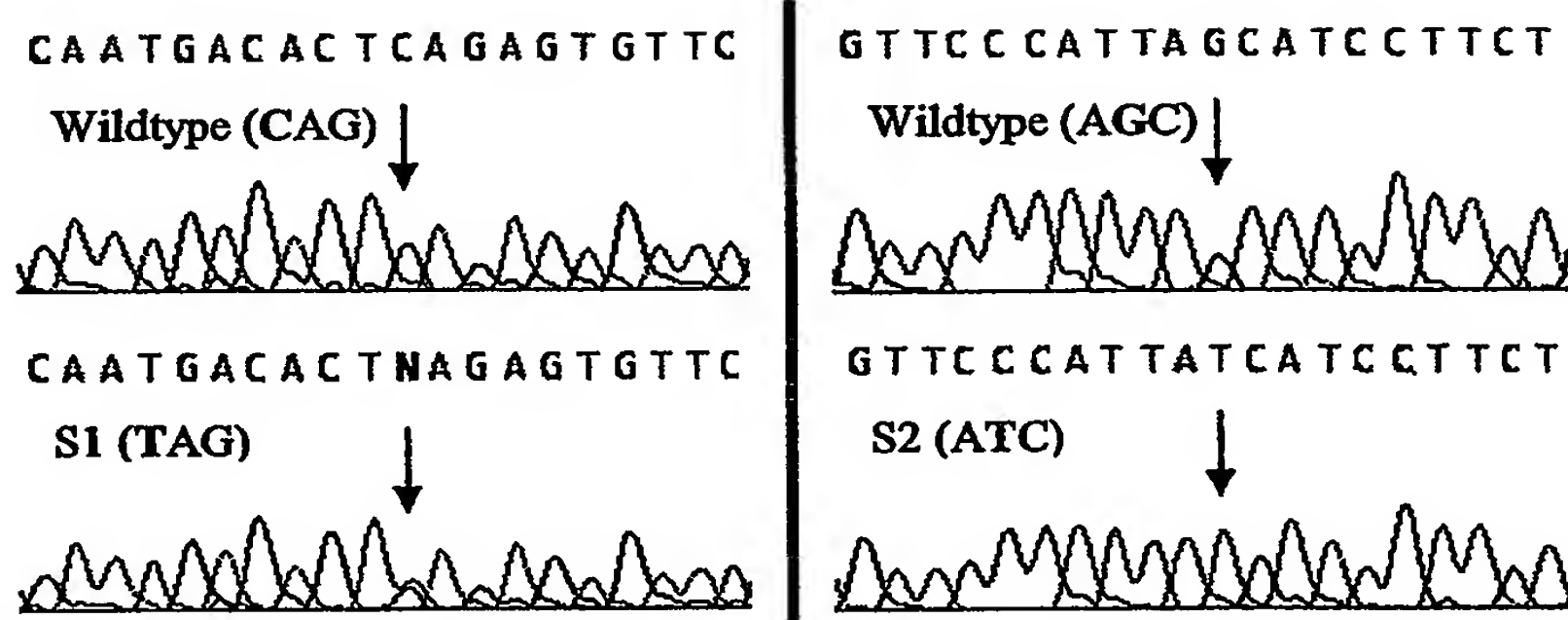
Figure 2b

Figure 3a

Animal		R 8 3 0	9 3 0 4 5 8	9 3 0 4 5 9	9 7 0 4	9 3 0 8 1 1	9 3 0 8 1 2	8 7 8 3	9 3 0 8 1 0	9 4 8 3 0 2	7 8 1 0
Phenotype Sterile (S) Fertile (F)		n/a	S	S	F	S	S	F	F	F	F
G E N O T Y P E	S1	+/Y	S1/+	S1/+	S1/+	+/+	+/+	+/+	+/+	+/+	+/+
	S2	S2/Y	S2/+	S2/+	+/+	S2/+	S2/+	+/+	S2/+	S2/+	+/+
	787	T/+	T/+	+/+	+/+	T/T	T/T	T/+	+/+	+/+	+/+

Figure 3b

Animal		962101	997634	997635	962152	997552	997553	976234	930142	948093	8874
Phenotype Sterile (S) Fertile (F)		n/a	S	S	F	F	S	F	n/a	S	F
G E N O T Y P E	S1	S1/Y	S1/S1	S1/S1	S1/+	S1/+	S1/S1	S1/+	S1/Y	S1/+	+/+
	S2	+/Y	+/+	+/+	+/+	+/+	+/+	+/+	+/+	+/+	+/+
	787	T/+	T/T	T/T	T/+	T/+	T/+	+/+	T/T	T/T	T/+

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Figure 4

Sheep GDF9

atg gcg ctt ccc	aac aaa ttc ttc ctt	tgg ttt tgc tgc ttt	gcc	45
Met Ala Leu Pro	Asn Lys Phe Phe Leu	Trp Phe Cys Cys Phe	Ala	
-315	-310	-305		
tgg ctc tgt ttt	cct att agc ctt gat	tct ctg cct tct agg	gga	90
Trp Leu Cys Phe	Pro Ile Ser Leu Asp	Ser Leu Pro Ser Arg	Gly	
-300	-295	-290		
gaa gct cag att	gta gct agg act gcg	ttg gaa tct gag gct	gag	135
Glu Ala Gln Ile	Val Ala Arg Thr Ala	Leu Glu Ser Glu Ala	Glu	
-285	-280	-275		
act tgg tcc ttg	ctg aac cat tta ggt	ggg aga cac aga cct	ggt	180
Thr Trp Ser Leu	Leu Asn His Leu Gly	Gly Arg His Arg Pro	Gly	
-270	-265	-260		
ctc ctt tcc cct	ctc tta gag gtt ctg	tat gat ggg cac ggg	gaa	225
Leu Leu Ser Pro	Leu Leu Glu Val Leu	Tyr Asp Gly His Gly	Glu	
-255	-250	-245		
ccc ccc agg ctg	cag cca gat gac aga	gct ttg cgc tac atg	aag	270
Pro Pro Arg Leu	Gln Pro Asp Asp Arg	Ala Leu Arg Tyr Met	Lys	
-240	-235	-230		
agg ctc tat aag	gca tac gct acc aag	gag ggg acc cct aaa	tcc	315
Arg Leu Tyr Lys	Ala Tyr Ala Thr Lys	Glu Gly Thr Pro Lys	Ser	
-225	-220	-215		
aac aga cgc cac	ctc tac aac act gtt	cgg ctc ttc acc ccc	tgt	360
Asn Arg Arg His	Leu Tyr Asn Thr Val	Arg Leu Phe Thr Pro	Cys	
-210	-205	-200		
gct cag cac aag	cag gct cct ggg gac	ctg gcg gca gga acc	ttt	405
Ala Gln His Lys	Gln Ala Pro Gly Asp	Leu Ala Ala Gly Thr	Phe	
-195	-190	-185		
cca tca gtg gat	ctg ctg ttt aac ctg	gat cgt gtt act gtt	gtg	450
Pro Ser Val Asp	Leu Leu Phe Asn Leu	Asp Arg Val Thr Val	Val	
-180	-175	-170		
gaa cat tta ttc	aag tca gtc ttg ctg	tat act ttc aac aac	tcc	495
Glu His Leu Phe	Lys Ser Val Leu Leu	Tyr Thr Phe Asn Asn	Ser	
-165	-160	-155		
att tct ttt ccc	ttt cct gtt aaa tgt	ata tgc aac ctg gtg	ata	540
Ile Ser Phe Pro	Phe Pro Val Lys Cys	Ile Cys Asn Leu Val	Ile	
-150	-145	-140		
aaa gag cca gag	ttt tct agc aag act	ctc cct aga gct cca	tac	585
Lys Glu Pro Glu	Phe Ser Ser Lys Thr	Leu Pro Arg Ala Pro	Tyr	
-135	-130	-125		
tca ttt acc tat	aac tca cag ttt gaa	ttt aga aag aaa tac	aaa	630
Ser Phe Thr Tyr	Asn Ser Gln Phe Glu	Phe Arg Lys Lys Tyr	Lys	
-120	-115	-110		
tgg atg gag att	gat gtg acg gct cct	ctt gag cct ctg gtg	gcc	678
Trp Met Glu Ile	Asp Val Thr Ala Pro	Leu Glu Pro Leu Val	Ala	
-105	-100	-95		
		[324]		

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Figure 4 continued

cac aag agg aat att cac atg tct gta aat ttt aca tgt gcg <u>gaa</u> gac	726
His Lys Arg Asn Ile His Met Ser Val Asn Phe Thr Cys Ala <u>Glu</u> Asp	
-90 -85 -80	
cag ctg cag cat cct tca gcg cgg gac agc ctg ttt aac atg act ctt	774
Gln Leu Gln His Pro Ser Ala Arg Asp Ser Leu Phe Asn Met Thr Leu	
-75 -70 -65	
ctc gta gcg ccc tca ctg ctt ttg tat ctg aac gac aca agt gct cag	822
Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln	
-60 -55 -50 -45	
gct ttt cac agg tgg cat tcc ctc cac cct aaa agg aag cct tca cag	870
Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln	
-40 -35 -30	
ggt cct gac cag aag aga ggg cta tct gcc tac ccc gtg gga gaa gaa	918
Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu	
-25 -20 -15	
gct gct gag ggt gta aga tcg tcc cgt cac cgc aga gac cag gag agt	966
Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser	
-10 -5 -1 1	
<u>gcc</u> agc tct <u>gaa</u> ttg aag aag cct ctg <u>gtt</u> cca gct tca gtc aat ctg	1014
Ala Ser Ser Glu Leu Lys Lys Pro Leu <u>Val</u> Pro Ala Ser Val Asn Leu	
5 10 15 20	
agt gaa tac ttc aaa cag ttt ctt ttt ccc cag aat gaa tgt gag ctc	1062
Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu	
25 30 35	
cat gac ttt aga ctt agc ttt agt cag ctg aag tgg gac aac tgg att	1110
His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile	
40 45 50	
<u>gtg</u> gcc cca cac aaa tac aac cct cga tac tgt aaa ggg gac tgt ccc	1158
<u>Val</u> Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro	
55 60 65	
agg gcg gtc gga cat cgg tat ggc <u>tct</u> ccg gtt cac acc atg gtg cag	1206
Arg Ala Val Gly His Arg Tyr Gly <u>Ser</u> Pro Val His Thr Met Val Gln	
70 75 80	
aac atc atc cat gag aaa ctt gac tcc tca gtg cca aga cca tcc tgt	1254
Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys	
85 90 95 100	
gta cct gcc aag tat agc cct ttg agt gtt ttg gcc atc gag cct gat	1302
Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp	
105 110 115	
ggc tca atc gct tat aaa gaa tat gaa gat atg ata gcc act aag tgt	1350
Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys	
120 125 130	
acc tgt cgt taa cagactc ctgtcaagta aaaccatgag tgtcctggcc	1399
Thr Cys Arg STOP	
135	
agtgtaaatg ccgcgcc	1416



Figure 5

Sheep BMP15 full

.atg	gtc	ctc	ctg	agc	atc	ctt	aga	atc							27	
.Met	Val	Leu	Leu	Ser	Ile	Leu	Arg	Ile								
																-265	
																-260	
[Leu] deletion																	
ctt	ctt	tgg	gga	ctg	gtg	ctt	ttt	atg	gaa	cat	agg	gtc	caa	atg		72	
<u>Leu</u>	Leu	Trp	Gly	Leu	Val	Leu	Phe	Met	Glu	His	Arg	Val	Gln	Met			
																-255	
																-245	
aca	cag	gta	ggg	cag	ccc	tct	att	gcc	cac	ctg	cct	gag	gcc	cct		117	
Thr	Gln	Val	Gly	Gln	Pro	Ser	Ile	Ala	His	Leu	Pro	Glu	Ala	Pro			
																-240	
																-235	
acc	ttg	ccc	ctg	att	cag	gag	ctg	cta	gaa	gaa	gcc	cct	ggc	aag		162	
Thr	Leu	Pro	Leu	Ile	Gln	Glu	Leu	Leu	Glu	Glu	Ala	Pro	Gly	Lys			
																-225	
																-220	
cag	cag	agg	aag	ccg	cgg	gtc	tta	ggg	cat	ccc	tta	cgg	tat	atg		207	
Gln	Gln	Arg	Lys	Pro	Arg	Val	Leu	Gly	His	Pro	Leu	Arg	Tyr	Met			
																-210	
																-205	
ctg	gag	ctg	tac	cag	cgt	tca	gct	gac	gca	agt	gga	cac	cct	agg		252	
Leu	Glu	Leu	Tyr	Gln	Arg	Ser	Ala	Asp	Ala	Ser	Gly	His	Pro	Arg			
																-195	
																-190	
gaa	aac	cgc	acc	att	ggg	gcc	acc	atg	gtg	agg	ctg	gtg	agg	ccg		297	
Glu	Asn	Arg	Thr	Ile	Gly	Ala	Thr	Met	Val	Arg	Leu	Val	Arg	Pro			
																-180	
																-175	
																-170	
Intron position																	
ctg	gct	agt	gta	gca	agg	cct	ctc	aga	g	-----					gc		327
Leu	Ala	Ser	Val	Ala	Arg	Pro	Leu	Arg							Gly		
																	-165
																	-160
tcc	tgg	cac	ata	cag	acc	ctg	gac	ttt	cct	ctg	aga	cca	aac	cgg		372	
Ser	Trp	His	Ile	Gln	Thr	Leu	Asp	Phe	Pro	Leu	Arg	Pro	Asn	Arg			
																-155	
																-150	
gta	gca	tac	caa	cta	gtc	aga	gcc	act	gtg	gtt	tac	cgc	cat	cag		417	
Val	Ala	Tyr	Gln	Leu	Val	Arg	Ala	Thr	Val	Val	Tyr	Arg	His	Gln			
																-140	
																-135	
ctt	cac	cta	act	cat	tcc	cac	ctc	tcc	tgc	cat	gtg	gag	ccc	tgg		462	
Leu	His	Leu	Thr	His	Ser	His	Leu	Ser	Cys	His	Val	Glu	Pro	Trp			

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Figure 5 continued

cta cga ctc cgc ttc gtg tgt cag cag cca aga ggt agt gag gtt ctt	651
Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly Ser Glu Val Leu	
-65 -60 -55	
gag ttc tgg tgg cat ggc act tca tca ttg gac act gtc ttc ttg tta	699
Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr Val Phe Leu Leu	
-50 -45 -40	
[S1] [422]	
ctg tat ttc aat gac act <u>cag</u> agt gtt cag aag acc aaa cct ctc cct	747
Leu Tyr Phe Asn Asp Thr <u>Gln</u> Ser Val Gln Lys Thr Lys Pro Leu Pro	
-35 -30 -25 -20	
aaa ggc ctg aaa gag ttt aca gaa aaa gac cct tct ctt ctc ttg agg	795
Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser Leu Leu Leu Arg	
-15 -10 -5	
agg gct cgt caa gca ggc agt att gca tgc gaa gtt cct ggc ccc tcc	843
Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val Pro Gly Pro Ser	
-1 1 5 10	
agg gag cat gat ggg cct gaa agt aac cag tgt tcc ctc cac cct ttt	891
Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser Leu His Pro Phe	
15 20 *** 25	
caa gtc agc ttc cag cag ctg ggc tgg gat cac tgg atc att gct ccc	939
Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp Ile Ile Ala Pro	
30 *** 35 40 45	
cat ctc tat acc cca aac tac tgt aag gga gta tgt cct cgg gta cta	987
His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys Pro Arg Val Leu	
50 55 60	
cac tat ggt ctc aat tct ccc aat cat gcc atc atc cag aac ctt gtc	1035
His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile Gln Asn Leu Val	
65 70 75	
agt gag ctg gtg gat cag aat gtc cct cag cct tcc tgt gtc cct tat	1083
Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser Cys Val Pro Tyr	
80 85 90	
[S2]	
aag tat gtt ccc att <u>agc</u> atc ctt ctg att gag gca aat ggg agt atc	1131
Lys Tyr Val Pro Ile <u>Ser</u> Ile Leu Leu Ile Glu Ala Asn Gly Ser Ile	
95 100 105	
ttg tac aag gag tat gag ggt atg att gcc cag tcc tgc aca tgc agg	1179
Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser Cys Thr Cys Arg	
110 115 120 125	
tga cggcaaagggtgca	
STOP	

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Figure 6

BMP2 Human	QAKHKQRKRLKS-----SKRHPLYVDFS-DVGWND
BMP7/OP1 Human	STGSKQSRQNRSKTPKNQALRMANVAENSSSDQRQA--KKHELYVSFR-DLGWQD
GDF9 SHEEP	RDQESASSELKKPLVPASVNLSEYFKQFLFP----QNEELHDFRLSFS-QLKWDN
GDF9 Human	GOETVSSSELKKPLGPASFNLSEYFRQFLLP----QNEELHDFRLSFS-QLKWDN
GDF9 Mouse	GQKAIRSEAKGPLLTASFNLSEYFKQFLFP----QNEELHDFRLSFS-QLKWDN
GDF9B SHEEP	QAGSIASEVPGPSREHDGPE-----SNQSLHFPQVSFQ-QLGWDH
GDF9B Mouse	QACSIESDASCPSQEHGDSV-----NNO SLHPYKVSEH-QLGWDH
GDF9B Human	QADGISAEVTASSSKHSGPE-----NNO SLHFPQISFR-QLGWDH
TGFB2 Human	ALDAAYCFRNVQDN-----CLRPLYIDFKRDLGWK-
TGFB3 Human	ALDTNYCFRNLEEN-----CVRPLYIDFRQDLGWK-
TGFB1 Human	ALDTNYCFSSTEKN-----CVRQLYIDFRKDLGWK-
	0 10 20 30 40 50
BMP2 Human	WIVAPPGYHAFYHGE PFPLADHLNSTNHAIVQTLVNSVN-SKIPKAVPTELSAISM
BMP7/OP1 Human	WIIAPEGYAAAYGEAFPLNSYMNATNHAIVQTLVHFINPETVPKPAPTQLNAISV
GDF9 SHEEP	WIVAPHKYNPRYKGD PRAVGHRYGSPVHTMVQNI IHEKLDSSVPRPSVPAKYSPLSV
GDF9 Human	WIVAPHRYNPRYKGD PRAVGHRYGSPVHTMVQNI IYEKLDSSVPRPSVPAKYSPLSV
GDF9 Mouse	WIVAPHRYNPRYKGD PRAVRHRYGSPVHTMVQNI IYEKLDPSVPRPSVPGKYSPLSV
GDF9B SHEEP	WIIAPHLTYTPNYKGV PRVLHYGLNSPNHAIIONLVSELVDQNVQPSVPYKYVPIS
GDF9B Mouse	WIIAPRLTYTPNYKGI TRVLPYGLNSPNHAI IQSLVNELVNHSVPQPSVPYNFLPMSI
GDF9B Human	WIIAPPFYTPNYKGT LRVLRDGLNSPNHAIIONLINQLVDQSVPRPSVPYKYVPISV
TGFB2 Human	WIHEPKGYNANFAGAPYLWS---SDTQHSRVLSTYNTINPEASAPVSQDLEPLTI
TGFB3 Human	WVHEPKGYANFSGP PYLRS---ADTTHSTVLGLYNTLNPEASAPVPQDLEPLTI
TGFB1 Human	WIHEPKGYHANF LGP PYIWS---LDTQYSKVLALYNQHNPGASAAPVPQALEPLPI
	60 70 80 90 100 * 110
BMP2 Human	LYLDENEKVVVLKNYQDMVVEGGR
BMP7/OP1 Human	LYFDDSSNVILKKYRNMVVRAAGH
GDF9 SHEEP	LAIEPDGSIAYKEYEDMIATKTER
GDF9 Human	LTIEPDGSIAYKEYEDMIATKTER
GDF9 Mouse	LTIEPDGSIAYKEYEDMIATRTER
GDF9B SHEEP	LLIEANGSILYKEYEGMIAQSETR
GDF9B Mouse	LLIETNGSILYKEYEGMIAQSETR
GDF9B Human	LMIEANGSILYKEYEGMIAESRTER
TGFB2 Human	LYYIGK-TPKIEQLSNMIVKSKS
TGFB3 Human	LYYVGR-TPKVEQLSNMVVKS
TGFB1 Human	VYYVGR-KPKVEQLSNMIVRSKS
	120 130 140

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Figure 7

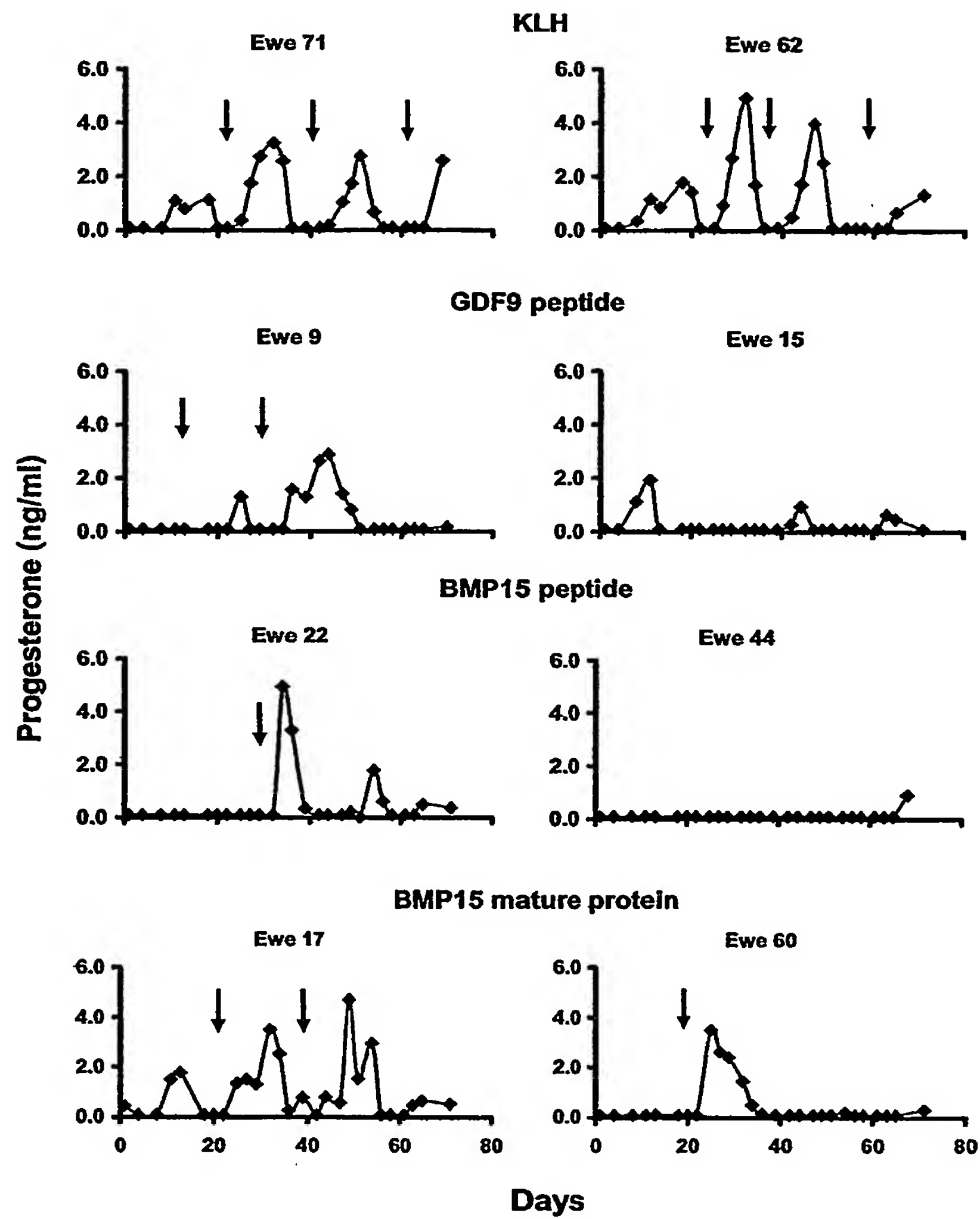


Figure 8

